**Amendments to the Claims:**

This listing of claims will replace all previous versions and listings of claims in the application:

1. (currently amended) A method of detecting of high-grade dysplasia (HGD) in cells of a human tissue sample, the method comprising:

(a) obtaining a test tissue sample suspected of comprising cells exhibiting HGD;

(b) establishing the level of expression in the test tissue sample of five genes:; AGR2 (SEO ID NO:3). TM7SFI (SEO ID NO: 13). MAT2B (SEO ID NO: 17), SLNAC I (SEO ID NO:23), and TCF4 (SEQ ID NO:43) or naturally occurring variants thereof, wherein the tissue is from esophagus or colon; and

(c) comparing expression of the five genes or naturally occurring variants thereof to a baseline expression of the genes or naturally occurring variants in normal tissue controls of the same tissue type, wherein an increase of at least 1.5-fold in expression of the genes relative to the baseline expression indicates that cells of the test sample exhibit HGD.

2. (canceled)

3. (currently amended) The method of claim 1, wherein the tissue is ~~A method of identifying~~ a esophageal tissue susceptible to esophageal adenocarcoma~~, comprising detecting esophageal HGD in a test tissue sample according to claim 1~~.

4. (previously presented) A method according to claim 1, wherein an increase of at least 2-fold in expression of genes relative to the baseline is observed.

5. (canceled)

6. (currently amended) A method for determining predisposition of a ~~mammalian~~ human tissue to a neo-plastic transformation by detecting HGD in cells of the tissue, the method comprising determining in a cell from the tissue expression of a nucleic acid sequence of five genes: AGR2 (SEQ ID NO:3), TM7SFI (SEQ ID NO: 13), MAT2B (SEO ID NO: 17), SLNAC I

(SEQ ID NO:23), and TCF4 (SEO ID NO:43) or naturally occurring variants thereof, wherein the tissue is from esophagus or colon; and ~~wherein the tissue of from esophagus or colon, and~~ wherein the expression in the test sample is at least 1.5-fold above baseline expression in a normal tissue control of the same tissue type.

7-8. (canceled)

9. (currently amended) A method of detecting of high-grade dysplasia (HGD) in cells of a human tissue sample, the method comprising:

(a) obtaining a test tissue sample suspected of comprising cells exhibiting HGD;

(b) establishing the level of expression in the test tissue sample of five polypeptides encoded by genes; AGR2 (SEO ID NO:3). TM7SFI (SEO ID NO: 13). MAT2B (SEO ID NO: 17), SLNAC I (SEO ID NO:23), and TCF4 (SEQ ID NO:43) or naturally occurring variants thereof, wherein the tissue is from esophagus or colon; and

(c) comparing expression of the five polypeptides or naturally occurring variants thereof in the test tissue sample to expression of the ~~at least eight~~ five polypeptides or naturally occurring variants thereof in normal tissue controls of the same tissue type, wherein an increase of at least 1.5-fold in expression of the polypeptides or naturally occurring variants in the test tissue sample relative to the normal tissue controls indicates that cells of the test sample exhibit HGD.

10. (currently amended) A method ~~as~~ according to claim 9 comprising contacting the test tissue sample with an antibody that specifically binds one of the ~~at least eight~~ five polypeptides under conditions that permit the antibody to bind the polypeptide.

11. (canceled)

12. (previously presented) The method of claim 1, wherein gene expression is determined by nucleic acid microarray analysis.

13. (currently amended) The method of claim 12, wherein the analysis comprises contacting nucleic acid from a test tissue sample with a nucleic acid microarray comprising nucleic acid probe sequences, wherein the nucleic acid probe sequences separately ~~comprises~~ comprise at least 50 contiguous nucleotides from five genes: AGR2 (SEQ ID N0:3), TM7SF1 (SEQ ID NO: 13), MAT2B (SEQ ID NO: 17). SLNAC1 (SEQ ID NO:23). and TCF4 (SEQ ID NO:43) or naturally occurring variants thereof.

14. (currently amended) The method of claim 13, wherein the ~~at least eight~~ nucleic acid probe sequences comprise at least 60 contiguous nucleotides ~~from a gene selected from the group~~.

15. (currently amended) The method of claim 14, wherein the ~~at least eight~~ nucleic acid probe sequences comprise at least 80 contiguous nucleotides ~~from a gene selected from the group~~.

16. (currently amended) The method of claim 15, wherein the ~~at least eight~~ nucleic acid probe sequences comprise at least 100 contiguous nucleotides ~~from a gene selected from the group~~.

17. (currently amended) The method of claim 16, wherein the ~~at least eight~~ nucleic acid probe sequences comprise at least 150 contiguous nucleotides ~~from a gene selected from the group~~.

18. (currently amended) The method of claim 17, wherein the ~~at least eight~~ nucleic acid probe sequences comprise at least 200 contiguous nucleotides ~~from a gene selected from the group~~.

19-24. (canceled)

25. (currently amended) The method of claim 1, wherein the level of expression of said five genes or naturally occurring variants thereof is established ~~gene expression is~~

~~determined~~ by nucleic acid hybridization under high stringency conditions of ~~a~~ detectable ~~probe~~ probes comprising at least 50 contiguous nucleotides from ~~a gene~~ said genes or or naturally occurring variants ~~selected from the group to nucleic acid of cells of the test tissue sample relative to cells of the normal tissue control~~.

26. (previously presented) The method of claim 25, wherein the hybridization is in *situ* hybridization.

27. (previously presented) The method of claim 26, wherein the hybridization is fluorescent in *situ* hybridization.

28. (previously presented) The method of claim 1, wherein gene expression is determined by polymerase chain reaction (PCR) analysis.

29. (previously presented) The method of claim 1, wherein gene expression is determined by real-time polymerase chain reaction (RT-PCR) analysis.

30. (previously presented) The method of claim 1, wherein gene expression is determined by Taqman® polymerase chain reaction analysis.

31-45. (canceled)